

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: HU, JING-SHAN
ROSEN, CRAIG A.
CAO, LIANG
- (ii) TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
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(C) CITY: WASHINGTON
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20005
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: TO BE ASSIGNED
(B) FILING DATE: HERewith
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/207,550
(B) FILING DATE: 8-MAR-1994
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/465,968
(B) FILING DATE: 06-JUN-1995
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
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(C) REFERENCE/DOCKET NUMBER: 1488.1000004
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1674 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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662220" 272599

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 12..80

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 81..1268

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 12..1268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCCTTCCAC C	ATG	CAC	TCG	CTG	GGC	TTC	TTC	TCT	GTG	GCG	TGT	TCT	CTG	50	
	Met	His	Ser	Leu	Gly	Phe	Phe	Ser	Val	Ala	Cys	Ser	Leu		
	-23			-20					-15						
CTC	GCC	GCT	GCG	CTG	CTC	CCG	GGT	CCT	CGC	GAG	GCG	CCC	GCC	GCC	98
Leu	Ala	Ala	Ala	Leu	Leu	Pro	Gly	Pro	Arg	Glu	Ala	Pro	Ala	Ala	
-10				-5						1				5	
GCC	GCC	TTC	GAG	TCC	GGA	CTC	GAC	CTC	TCG	GAC	GCG	GAG	CCC	GAC	146
Ala	Ala	Phe	Glu	Ser	Gly	Leu	Asp	Leu	Ser	Asp	Ala	Glu	Pro	Asp	
			10					15					20		
GGC	GAG	GCC	ACG	GCT	TAT	GCA	AGC	AAA	GAT	CTG	GAG	GAG	CAG	TTA	194
Gly	Glu	Ala	Thr	Ala	Tyr	Ala	Ser	Lys	Asp	Leu	Glu	Glu	Gln	Leu	
		25						30					35		
TCT	GTG	TCC	AGT	GTA	GAT	GAA	CTC	ATG	ACT	GTA	CTC	TAC	CCA	GAA	242
Ser	Val	Ser	Ser	Val	Asp	Glu	Leu	Met	Thr	Val	Leu	Tyr	Pro	Glu	
	40					45					50				
TGG	AAA	ATG	TAC	AAG	TGT	CAG	CTA	AGG	AAA	GGA	GGC	TGG	CAA	CAT	290
Trp	Lys	Met	Tyr	Lys	Cys	Gln	Leu	Arg	Lys	Gly	Gly	Trp	Gln	His	
55					60					65				70	
AGA	GAA	CAG	GCC	AAC	CTC	AAC	TCA	AGG	ACA	GAA	GAG	ACT	ATA	AAA	338
Arg	Glu	Gln	Ala	Asn	Leu	Asn	Ser	Arg	Thr	Glu	Glu	Thr	Ile	Lys	
				75					80					85	
GCT	GCA	GCA	CAT	TAT	AAT	ACA	GAG	ATC	TTG	AAA	AGT	ATT	GAT	AAT	386
Ala	Ala	Ala	His	Tyr	Asn	Thr	Glu	Ile	Leu	Lys	Ser	Ile	Asp	Asn	
			90					95					100		
TGG	AGA	AAG	ACT	CAA	TGC	ATG	CCA	CGG	GAG	GTG	TGT	ATA	GAT	GTG	434
Trp	Arg	Lys	Thr	Gln	Cys	Met	Pro	Arg	Glu	Val	Cys	Ile	Asp	Val	
		105					110					115			
AAG	GAG	TTT	GGA	GTC	GCG	ACA	AAC	ACC	TTC	TTT	AAA	CCT	CCA	TGT	482
Lys	Glu	Phe	Gly	Val	Ala	Thr	Asn	Thr	Phe	Phe	Lys	Pro	Pro	Cys	
			120				125				130				
TCC	GTC	TAC	AGA	TGT	GGG	GGT	TGC	TGC	AAT	AGT	GAG	GGG	CTG	CAG	530
Ser	Val	Tyr	Arg	Cys	Gly	Gly	Cys	Cys	Asn	Ser	Glu	Gly	Leu	Gln	
135					140				145					150	

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ATG AAC ACC AGC ACG AGC TAC CTC AGC AAG ACG TTA TTT GAA ATT ACA	578
Met Asn Thr Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr	
155 160 165	
GTG CCT CTC TCT CAA GGC CCC AAA CCA GTA ACA ATC AGT TTT GCC AAT	626
Val Pro Leu Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn	
170 175 180	
CAC ACT TCC TGC CGA TGC ATG TCT AAA CTG GAT GTT TAC AGA CAA GTT	674
His Thr Ser Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val	
185 190 195	
CAT TCC ATT ATT AGA CGT TCC CTG CCA GCA ACA CTA CCA CAG TGT CAG	722
His Ser Ile Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln	
200 205 210	
GCA GCG AAC AAG ACC TGC CCC ACC AAT TAC ATG TGG AAT AAT CAC ATC	770
Ala Ala Asn Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile	
215 220 225 230	
TGC AGA TGC CTG GCT CAG GAA GAT TTT ATG TTT TCC TCG GAT GCT GGA	818
Cys Arg Cys Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly	
235 240 245	
GAT GAC TCA ACA GAT GGA TTC CAT GAC ATC TGT GGA CCA AAC AAG GAG	866
Asp Asp Ser Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu	
250 255 260	
CTG GAT GAA GAG ACC TGT CAG TGT GTC TGC AGA GCG GGG CTT CGG CCT	914
Leu Asp Glu Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro	
265 270 275	
GCC AGC TGT GGA CCC CAC AAA GAA CTA GAC AGA AAC TCA TGC CAG TGT	962
Ala Ser Cys Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys	
280 285 290	
GTC TGT AAA AAC AAA CTC TTC CCC AGC CAA TGT GGG GCC AAC CGA GAA	1010
Val Cys Lys Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu	
295 300 305 310	
TTT GAT GAA AAC ACA TGC CAG TGT GTA TGT AAA AGA ACC TGC CCC AGA	1058
Phe Asp Glu Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg	
315 320 325	
AAT CAA CCC CTA AAT CCT GGA AAA TGT GCC TGT GAA TGT ACA GAA AGT	1106
Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser	
330 335 340	
CCA CAG AAA TGC TTG TTA AAA GGA AAG AAG TTC CAC CAC CAA ACA TGC	1154
Pro Gln Lys Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys	
345 350 355	
AGC TGT TAC AGA CGG CCA TGT ACG AAC CGC CAG AAG GCT TGT GAG CCA	1202
Ser Cys Tyr Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro	
360 365 370	
GGA TTT TCA TAT AGT GAA GAA GTG TGT CGT TGT GTC CCT TCA TAT TGG	1250
Gly Phe Ser Tyr Ser Glu Gln Val Cys Arg Cys Val Pro Ser Tyr Trp	
375 380 385 390	
CAA AGA CCA CAA ATG AGC TAAGATTGTA CTGTTTTCCA GTTCATCGAT	1298

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Gln Arg Pro Gln Met Ser
395

TTTCTATTAT GGAAACTGT GTTGCCACAG TAGAACTGTC TGTGAACAGA GAGACCCTTG 1358
TGGGTCCATG CTAACAAAGA CAAAAGTCTG TCTTTCCTGA ACCATGTGGA TAACTTTACA 1418
GAAATGGACT GGAGCTCATC TGCAAAAGGC CTCTTGTAAG GACTGGTTTT CTGCCAATGA 1478
CCAAACAGCC AAGATTTTCC TCTTGTGATT TCTTTAAAAG AATGACTATA TAATTTATTT 1538
CCACTAAAAA TATTGTTTCT GCATTCATTT TTATAGCAAC AACAAATTGGT AAAACTCACT 1598
GTGATCAATA TTTTATATC ATGCAAAATA TGTTTAAAAT AAAATGAAAA TTGTATTTAT 1658
AAAAAAAAAA AAAAAA 1674

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	His	Ser	Leu	Gly	Phe	Phe	Ser	Val	Ala	Cys	Ser	Leu	Leu	Ala	Ala	
-23			-20					-15						-10		
Ala	Leu	Leu	Pro	Gly	Pro	Arg	Glu	Ala	Pro	Ala	Ala	Ala	Ala	Ala	Phe	
		-5					1				5					
Glu	Ser	Gly	Leu	Asp	Leu	Ser	Asp	Ala	Glu	Pro	Asp	Ala	Gly	Glu	Ala	
10				15					20					25		
Thr	Ala	Tyr	Ala	Ser	Lys	Asp	Leu	Glu	Glu	Gln	Leu	Arg	Ser	Val	Ser	
				30				35						40		
Ser	Val	Asp	Glu	Leu	Met	Thr	Val	Leu	Tyr	Pro	Glu	Tyr	Trp	Lys	Met	
		45						50					55			
Tyr	Lys	Cys	Gln	Leu	Arg	Lys	Gly	Gly	Trp	Gln	His	Asn	Arg	Glu	Gln	
		60					65					70				
Ala	Asn	Leu	Asn	Ser	Arg	Thr	Glu	Glu	Thr	Ile	Lys	Phe	Ala	Ala	Ala	
	75					80					85					
His	Tyr	Asn	Thr	Glu	Ile	Leu	Lys	Ser	Ile	Asp	Asn	Glu	Trp	Arg	Lys	
90					95					100					105	
Thr	Gln	Cys	Met	Pro	Arg	Glu	Val	Cys	Ile	Asp	Val	Gly	Lys	Glu	Phe	
			110					115						120		
Gly	Val	Ala	Thr	Asn	Thr	Phe	Phe	Lys	Pro	Pro	Cys	Val	Ser	Val	Tyr	
			125					130					135			
Arg	Cys	Gly	Gly	Cys	Cys	Asn	Ser	Glu	Gly	Leu	Gln	Cys	Met	Asn	Thr	
		140					145					150				

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Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
155 160 165

Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
170 175 180 185

Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
190 195 200

Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
205 210 215

Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
220 225 230

Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
235 240 245

Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
250 255 260 265

Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
270 275 280

Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
285 290 295

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
300 305 310

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
315 320 325

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
330 335 340 345

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
350 355 360

Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
365 370 375

Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Gln Arg Pro
380 385 390

Gln Met Ser
395

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1526 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: sig_peptide

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(B) LOCATION: 71..142

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 143..1120

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 71..1120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGAGGCCACG GCTTATGCAA GCAAAGATCT GGAGGAGCAG TTACGGTCTG TGTCCAGTGT	60
AGATGAACTC ATG ACT GTA CTC TAC CCA GAA TAT TGG AAA ATG TAC AAG	109
Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys	
-24 -20 -15	
TGT CAG CTA AGG AAA GGA GGC TGG CAA CAT AAC AGA GAA CAG GCC AAC	157
Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln Ala Asn	
-10 -5 1 5	
CTC AAC TCA AGG ACA GAA GAG ACT ATA AAA TTT GCT GCA GCA CAT TAT	205
Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr	
10 15 20	
AAT ACA GAG ATC TTG AAA AGT ATT GAT AAT GAG TGG AGA AAG ACT CAA	253
Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln	
25 30 35	
TGC ATG CCA CGG GAG GTG TGT ATA GAT GTG GGG AAG GAG TTT GGA GTC	301
Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val	
40 45 50	
GCG ACA AAC ACC TTC TTT AAA CCT CCA TGT GTG TCC GTC TAC AGA TGT	349
Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys	
55 60 65	
GGG GGT TGC TGC AAT AGT GAG GGG CTG CAG TGC ATG AAC ACC AGC ACG	397
Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr	
70 75 80 85	
AGC TAC CTC AGC AAG ACG TTA TTT GAA ATT ACA GTG CCT CTC TCT CAA	445
Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln	
90 95 100	
GGC CCC AAA CCA GTA ACA ATC AGT TTT GCC AAT CAC ACT TCC TGC CGA	493
Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg	
105 110 115	
TGC ATG TCT AAA CTG GAT GTT TAC AGA CAA GTT CAT TCC ATT ATT AGA	541
Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg	
120 125 130	
CGT TCC CTG CCA GCA ACA CTA CCA CAG TGT CAG GCA GCG AAC AAG ACC	589
Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr	
135 140 145	
TGC CCC ACC AAT TAC ATG TGG AAT AAT CAC ATC TGC AGA TGC CTG GCT	637
Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys Leu Ala	

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150	155	160	165	
CAG GAA GAT TTT ATG TTT TCC TCG GAT GCT GGA GAT GAC TCA ACA GAT				685
Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser Thr Asp	170	175	180	
GGA TTC CAT GAC ATC TGT GGA CCA AAC AAG GAG CTG GAT GAA GAG ACC				733
Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr	185	190	195	
TGT CAG TGT GTC TGC AGA GCG GGG CTT CGG CCT GCC AGC TGT GGA CCC				781
Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys Gly Pro	200	205	210	
CAC AAA GAA CTA GAC AGA AAC TCA TGC CAG TGT GTC TGT AAA AAC AAA				829
His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys Asn Lys	215	220	225	
CTC TTC CCC AGC CAA TGT GGG GCC AAC CGA GAA TTT GAT GAA AAC ACA				877
Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr	230	235	240	245
TGC CAG TGT GTA TGT AAA AGA ACC TGC CCC AGA AAT CAA CCC CTA AAT				925
Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn	250	255	260	
CCT GGA AAA TGT GCC TGT GAA TGT ACA GAA AGT CCA CAG AAA TGC TTG				973
Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu	265	270	275	
TTA AAA GGA AAG AAG TTC CAC CAC CAA ACA TGC AGC TGT TAC AGA CGG				1021
Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg	280	285	290	
CCA TGT ACG AAC CGC CAG AAG GCT TGT GAG CCA GGA TTT TCA TAT AGT				1069
Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser	295	300	305	
GAA GAA GTG TGT CGT TGT GTC CCT TCA TAT TGG CAA AGA CCA CAA ATG				1117
Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Gln Arg Pro Gln Met	310	315	320	325
AGC TAAGATTGTA CTGTTTTCCA GTTCATCGAT TTTCTATTAT GGAAACTGT				1170
Ser				
GTTGCCACAG TAGAACTGTC TGTGAACAGA GAGACCCTTG TGGGTCCATG CTAACAAAGA				1230
CAAAAGTCTG TCTTTCCTGA ACCATGTGGA TAACTTTACA GAAATGGACT GGAGCTCATC				1290
TGCAAAAGGC CTCTTGTAAG GACTGGTTTT CTGCCAATGA CCAAACAGCC AAGATTTTCC				1350
TCTTGTGATT TCTTTAAAAG AATGACTATA TAATTTATTT CCACTAAAAA TATTGTTTCT				1410
GCATTCATTT TTATAGCAAC AACAATTGGT AAAACTCACT GTGATCAATA TTTTATATC				1470
ATGCAAAATA TGTTTAAAAT AAAATGAAAA TTGTATTTAT AAAAAAAAAA AAAAAA				1526

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys Cys Gln Leu
-24 -20 -15 -10

Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln Ala Asn Leu Asn Ser
-5 1 5

Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr Asn Thr Glu
10 15 20

Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met Pro
25 30 35 40

Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val Ala Thr Asn
45 50 55

Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys
60 65 70

Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Ser Tyr Leu
75 80 85

Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly Pro Lys
90 95 100

Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met Ser
105 110 115 120

Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg Ser Leu
125 130 135

Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr Cys Pro Thr
140 145 150

Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys Leu Ala Gln Glu Asp
155 160 165

Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser Thr Asp Gly Phe His
170 175 180

Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr Cys Gln Cys
185 190 195 200

Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys Gly Pro His Lys Glu
205 210 215

Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys Asn Lys Leu Phe Pro
220 225 230

Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr Cys Gln Cys
235 240 245

Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn Pro Gly Lys

250		255		260	
Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu Leu Lys Gly					
265		270		275	280
Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg Pro Cys Thr					
	285		290		295
Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser Glu Glu Val					
	300		305		310
Cys Arg Cys Val Pro Ser Tyr Trp Gln Arg Pro Gln Met Ser					
	315		320		325

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Arg Thr Leu Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala					
1	5		10		15
His Val Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg					
	20		25		30
Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu					
	35		40		45
Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg					
	50		55		60
Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu					
	65		70		75
Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys					
	85		90		95
Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro					
	100		105		110
Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg					
	115		120		125
Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg					
	130		135		140
Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys					
	145		150		155
Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu					
	165		170		175

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Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp
 180 185 190
 Thr Asp Val Arg
 195

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 241 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Asn Arg Cys Trp Ala Leu Phe Leu Ser Leu Cys Cys Tyr Leu Arg
 1 5 10 15
 Leu Val Ser Ala Glu Gly Asp Pro Ile Pro Glu Glu Leu Tyr Glu Met
 20 25 30
 Leu Ser Asp His Ser Ile Arg Ser Phe Asp Asp Leu Gln Arg Leu Leu
 35 40 45
 His Gly Asp Pro Gly Glu Glu Asp Gly Ala Glu Leu Asp Leu Asn Met
 50 55 60
 Thr Arg Ser His Ser Gly Gly Glu Leu Glu Ser Leu Ala Arg Gly Arg
 65 70 75 80
 Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala Glu
 85 90 95
 Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp
 100 105 110
 Arg Thr Asn Ala Asn Phe Leu Val Trp Pro Pro Cys Val Glu Val Gln
 115 120 125
 Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro Thr
 130 135 140
 Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val Arg
 145 150 155 160
 Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His Leu
 165 170 175
 Ala Cys Lys Cys Glu Thr Val Ala Ala Ala Arg Pro Val Thr Arg Ser
 180 185 190
 Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys Thr Pro Gln Thr Arg Val
 195 200 205
 Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His Arg

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210		215		220
Lys Phe Lys His Thr His Asp Lys Thr Ala Leu Lys Glu Thr Leu Gly				
225		230	235	240
Ala				

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 232 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu		
1	5	10 15
Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly		
	20	25 30
Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln		
	35	40 45
Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu		
	50	55 60
Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu		
	65	70 75 80
Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro		
	85	90 95
Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His		
	100	105 110
Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys		
	115	120 125
Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val		
	130	135 140
Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Tyr		
	145	150 155 160
Lys Ser Trp Ser Val Tyr Val Gly Ala Arg Cys Cys Leu Met Pro Trp		
	165	170 175
Ser Leu Pro Gly Pro His Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys		
	180	185 190
His Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn		
	195	200 205

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Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr
210 215 220

Cys Arg Cys Asp Lys Pro Arg Arg
225 230

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Pro Xaa Cys Val Xaa Xaa Xaa Arg Cys Xaa Gly Cys Cys Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGCTTCCGG CTCGTATG

18

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGTTTTCCC AGTCACGAC

18

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:

00257272 022599

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCACATGGTT CAGGAAAGAC A

21

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGTAATACGA CTCACTATAG GGATCCCGCC ATGGAGGCCA CGGCTTATGC

50

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATCTCTAGA TTAGCTCATT TGTGGTCT

28

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGCGGATCCA TGACTGTACT CTACCCA

27

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCTCTAGAT CAAGCGTAGT CTGGGACGTC GTATGGGTAC TCGAGGCTCA TTTGTGGTCT

60

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